

18/484312

Fig.1/1

GAATTCTCTGGACTGAGGCTCCAGTTCTGGCCTTGGGG

TTCAAGATCACTGGGACCAGGCCGTGATCTATGCCCGAGTCTAACCCCTAACTGTC
ACCCCAAGGCACTTGGGACGTCCCTGGACAGACCGAGTCCGGAAAGCCCCAGCACTGCC

GCTGCCACACTGCCCTGAGCCCAAATGGGGAGTGAGAGGCCA TAG CTG TCT GGC

S1	S5	S10	S15
Met Gly Leu Ser Thr Val Pro Asp	Leu Leu Leu Pro Leu Val	Leu	
ATG GGC CTC TCC ACC GTG CCT GAC	CTG CTG CCA CTG GTG CTC		
216 225 234	243	252	

S20	S25	S29	1
Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu			
CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG			
261 270 279	288	297	

5	10	15	
Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro			
GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC			
306 315 324	333	342	

20	25	30	
Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr			
CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC			
351 360 369	378	387	

35	40	45	
Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro			
AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG			
396 405 414	423	432	

50	55	60	
Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr			
GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC			
441 450 459	468	477	

65	70	75	
Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys			
GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC			
486 495 504	513	522	

80	85	90	
Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp			
CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TGC ACA GTG GAC			
531 540 549	558	567	

95	100	105	
Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr			
CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT			
576 585 594	603	612	

110	115	120	
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu			
TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC			
621 630 639	648	657	

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Fig.1/2

125	130	135
Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val		
AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG		
666 675 684 693 702		
140	145	150
Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val		
TGC ACC TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC		
711 720 729 738 747		
155	160	165
Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys		
TCC TGT AGT AAC TGT AAG AAA AGC CTG GAG TGC ACG AAG TTG TGC		
756 765 774 783 792		
170	175	180
Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr		
CTA CCC CAG ATT GAG AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC		
801 810 819 828 837		
185	190	195
Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu		
ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT GGT CTT TGC CTT TTA		
846 855 864 873 882		
200	205	210
Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys		
TCC CTC CTC TTC ATT GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG		
891 900 909 918 927		
215	220	225
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys		
TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA TCG ACA CCT GAA AAA		
936 945 954 963 972		
230	235	240
Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn		
GAG GGG GAG CTT GAA GGA ACT ACT ACT AAG CCC CTG GCC CCA AAC		
981 990 999 1008 1017		
245	250	255
Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe		
CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC CCC ACC CTG GGC TTC		
1026 1035 1044 1053 1062		
260	265	270
Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr		
AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC		
1071 1080 1089 1098 1107		
275	280	285
Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala		
CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA		
1116 1125 1134 1143 1152		

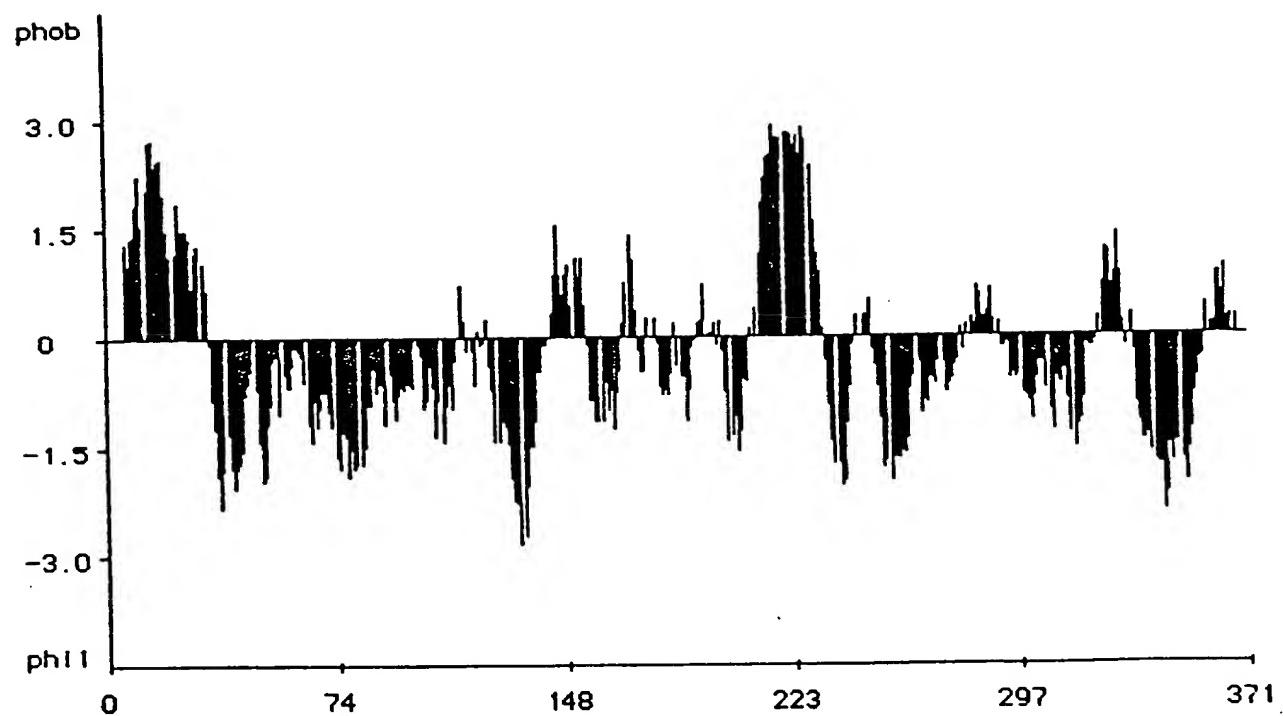
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Fig.1/3

290	295	300
Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala		
CCA CCC TAT CAG GGG GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC		
1161 1170 1179	1188	1197
305	310	315
Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala		
TCC GAC CCC ATC CCC AAC CCC CTT CAG AAG TGG GAG GAC AGC GCC		
1206 1215 1224	1233	1242
320	325	330
His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr		
CAC AAG CCA CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC		
1251 1260 1269	1278	1287
335	340	
Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp		
GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC TGG AA <u>GGAATTG</u>		
1296 1305 1314	1323	1332

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Fig.2



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Fig. 3

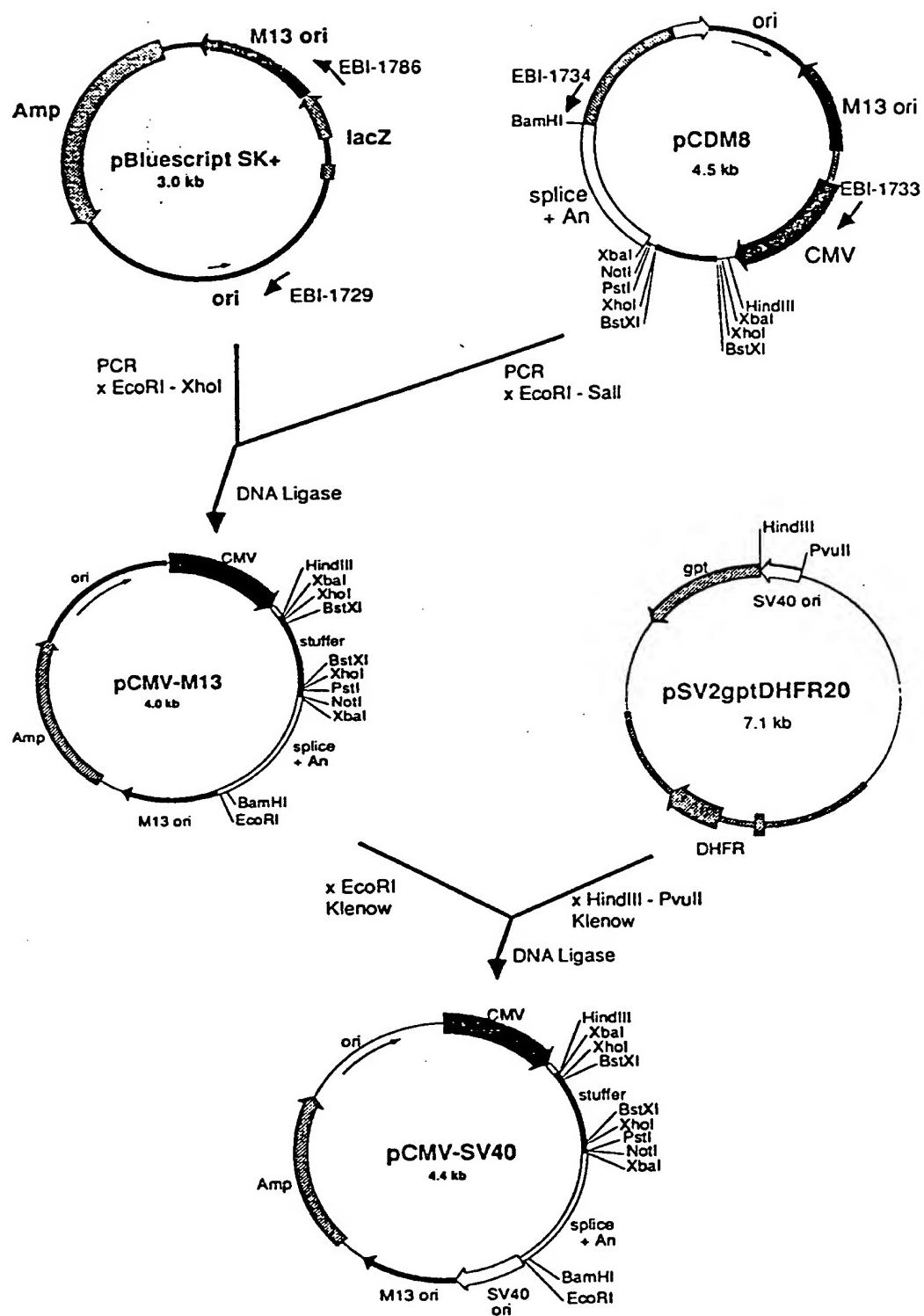


Fig. 4

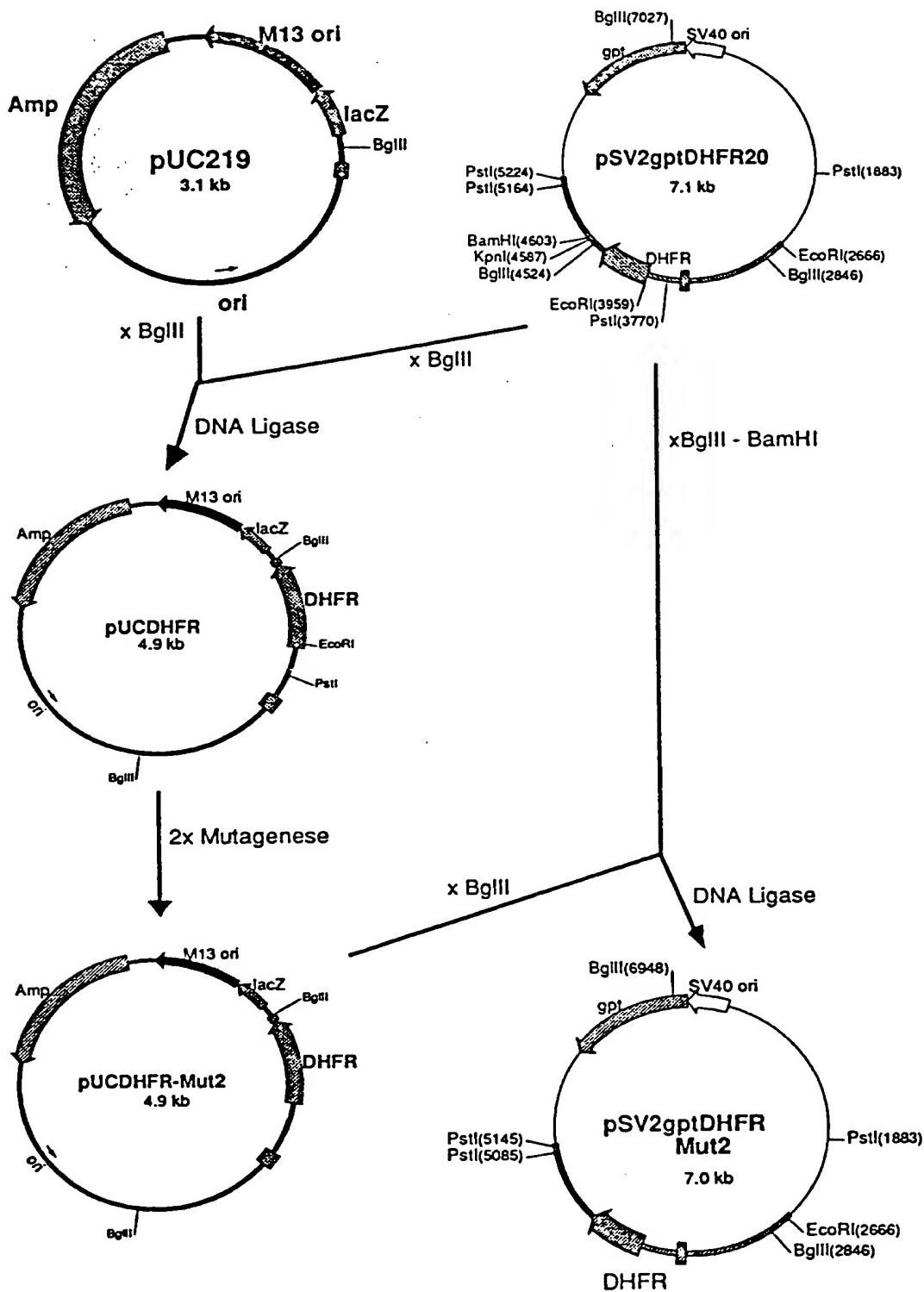


Fig.5

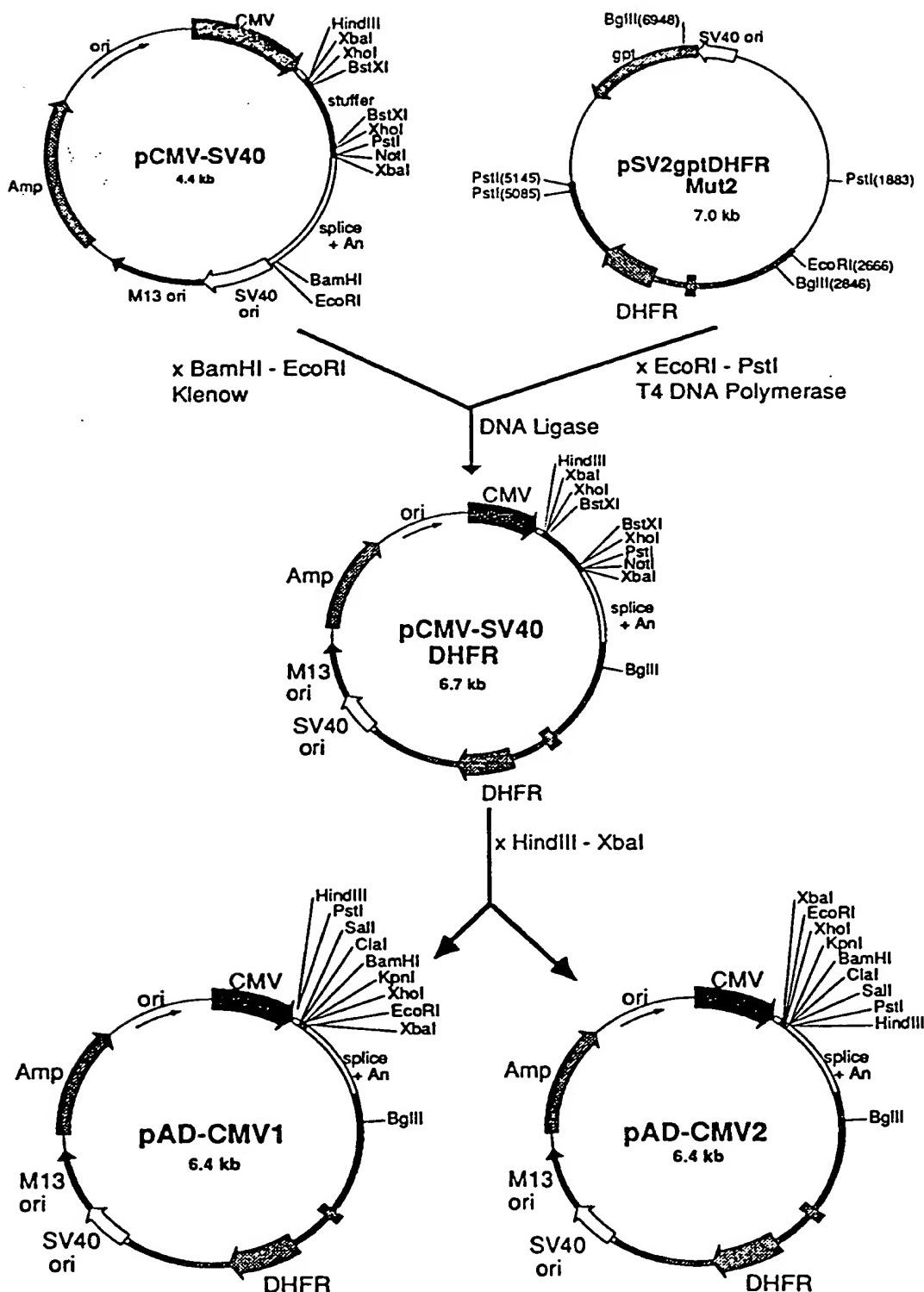


Fig. 6/1

pAD-CMV1 : 6414 bp

TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTCAT TAGTTCATAG	60
CCCATATATG GAGTTCCCGCG TTACATAACT TACGGTAAAT GGCCCGCCTG GCTGACCGCC	120
CAACGACCCC CGCCCATTGA CGTCAATAAT GACGTATGTT CCCATAGTAA CGCCAATAGG	180
GACTTTCCAT TGACGTCAAT GGGTGGAGTA TTTACGGTAA ACTGCCACT TGGCAGTACA	240
TCAAGTGTAT CATATGCCAA GTACGCCCCC TATTGACGTC AATGACGGTA AATGGCCCGC	300
CTGGCATTAT GCCCAGTACA TGACCTTATG GGACTTCCCT ACTGGCAGT ACATCTACGT	360
ATTAGTCATC GCTATTACCA TGGTGATGCG GTTTGGCAG TACATCAATG GGCGTGGATA	420
GCGGTTTGAC TCACGGGGAT TTCCAAGTCT CCACCCATT GACGTCAATG GGAGTTGTT	480
TTGGCACCAA AATCAACGGG ACTTTCCAAA ATGTCGTAAC AACTCCGCC CATTGACGCA	540
AATGGGCAGT AGGCGTGTAC GGTGGGAGGT CTATATAAGC AGAGCTCTCT GGCTAACTAG	600
AGAACCCACT GCTTAACCTGG CTTATCGAAA TTAATACGAC TCACTATAGG GAGACCCAAG	660
CTTCTGCAGG TCGACATCGA TGGATCCGGT ACCTCGAGCG CGAATTCTCT AGAGGATCTT	720
TGTGAAGGAA CCTTACTTCT GTGGTGTGAC ATAATTGGAC AAACTACCTA CAGAGATTAA	780
AAGCTCTAAG GTAAATATAA AATTTTAAG TGTATAATGT GTTAAACTAC TGATTCTAAT	840
TGTTTGTGTA TTTTAGATTC CAACCTATGG AACTGATGAA TGGGAGCAGT GGTGGAATGC	900
CTTTAATGAG GAAAACCTGT TTTGCTCAGA AGAAATGCCA TCTAGTGATG ATGAGGCTAC	960
TGCTGACTCT CAACATTCTA CTCCTCCAAA AAAGAAGAGA AAGGTAGAAG ACCCCAAGGA	1020
CTTCCTTCA GAATTGCTAA GTTTTTGAG TCATGCTGTG TTTAGTAATA GAACTCTTGC	1080
TTGCTTGCT ATTTACACCA CAAAGGAAAA AGCTGCACTG CTATACAAGA AAATTATGGA	1140
AAAATATTG ATGTATAGTG CCTTGACTAG AGATCATAAT CAGCCATACC ACATTTGTAG	1200
AGGTTTACT TGCTTTAAAA AACCTCCAC ACCTCCCCCT GAACCTGAAA CATAAAATGA	1260
ATGCAATTGT TGTTGTTAAC TTGTTTATTG CAGCTTATAA TGGTTACAAA TAAAGCAATA	1320
GCATCACAAA TTTCACAAAT AAAGCATTTC TTTCACTGCA TTCTAGTTGT GGTTTGTCCA	1380
AACTCATCAA TGTATCTTAT CATGTCTGGA TCAATTCTGA GAAACTAGCC TTAAAGACAG	1440
ACAGCTTGCT TCTAGTCAGC CAGGCAAGCA TATGTAATAA AAGTTCTCA GGGAACTGAG	1500
GTAAAAGAT GTATCCTGGA CCTGCCAGAC CTGGCCATTC ACGTAAACAG AAGATTCCGC	1560
CTCAAGTTCC GGTTAACAAAC AGGAGGCAAC GAGATCTCAA ATCTATTACT TCTAATCGGG	1620
TAATTAAAAC CTTCAACTA AAACACGGAC CCACGGATGT CACCCACTTT TCCTTCCCCG	1680
GCTCCGCCCT TCTCAGTACT CCCCCACCATT AGGCTCGCTA CTCCACCTCC ACTTCCGGC	1740

Fig.6/2

GCGACACCCA CGTGCCCTCT CCCACCCGAC GCTAACCCCG CCCCTGCCCG TCTGACCCCG	1800
CCCACCACCT GGCCCCGCC CGTTGAGGAC AGAAGAAACC CCGGGCAGCC GCAGCCAAGG	1860
CGGACGGGTA GACGCTGGGG GCGCTGAGGA GTCGTCCTCT ACCTTCTCTG CTGGCTCGGT	1920
GGGGGACGCG GTGGATCTCA GGCTTCCGGA AGACTGGAAG AACCGGCTCA GAACCGCTTG	1980
TCTCCGCGGG GCTTGGCGG CGGAAGAATG GCCGCTAGAC GCGGACTTGG TGCGAGGCAT	2040
CGCAGGATGC AGAAGAGCAA GCCCGCCGGG AGCGCGCGGC TGTACTACCC CGCGCCTGGA	2100
GCGGCACGC CGGACTGGC GGGGCCGGCC TGGTGGAGGC GGAGTCTGAC CTCGTGGAGG	2160
CGGGGCCTCT GATGTTCAAA TAGGATGCTA GGCTTGTGAA GGCGTGGCCT CCGATTACACA	2220
AGTGGGAAGC AGCGCCGGC GACTGCAATT TCGCGCCAAA CTTGGGGAA GCACAGCGTA	2280
CAGGCTGCCT AGGTGATCGC TGCTGCTGTC ATGGTTCGAC CGCTGAAC TG CATCGTCGCC	2340
GTGTCCCAGA ATATGGGCAT CGGCAAGAAC GGAGACCTTC CCTGGCCAAT GCTCAGGTAC	2400
TGGCTGGATT GGGTTAGGGA AACCGAGGCG GTTCGCTGAA TCGGGTCGAG CACTTGGCGG	2460
.AGACGCGCGG GCCAACTACT TAGGGACAGT CATGAGGGGT AGGCCCCCG GCTGCTGCC	2520
TTGCCCATGC CCGCGGTGAT CCCCATGCTG TGCCAGCCTT TGCCCAGAGG CGCTCTAGCT	2580
GGGAGCAAAG TCCGGTCACT GGGCAGCACC ACCCCCCGGA CTTGCATGGG TAGCCGCTGA	2640
GATGGAGCCT GAGCACACGT GACAGGGTCC CTGTTAACGC AGTGTTCCTC TAACTTTCAG	2700
GAACGAGTTC AAGTACTTCC AAAGAATGAC CACCACCTCC TCAGTGGAAAG GTAAACAGAA	2760
CCTGGTGATT ATGGGCCGGA AAACCTGGTT CTCCATTCCCT GAGAAGAAC GACCTTTAAA	2820
GGACAGAATT AATATAGTTC TCAGTAGAGA GCTCAAGGAA CCACCACAAG GAGCTCATT	2880
TCTTGCCAAA AGTCTGGACC ATGCCTTAAA ACTTATTGAA CAACCAGAGT TAGCAGATAA	2940
AGTGGACATG GTTTGGATAG TTGGAGGCAG TTCCGTTAC AAGGAAGCCA TGAATCAGCC	3000
AGGCCATCTC AGACTCTTG TGACAAGGAT CATGCAGGAA TTTGAAAGTG ACACGTTCTT	3060
CCCAGAAATT GATTTGGAGA AATATAAACT TCTCCCAGAG TACCCAGGGG TCCTTCTGA	3120
AGTCCAGGAG GAAAAAGGCA TCAAGTATAA ATTGAAGTC TATGAGAAGA AAGGCTAAC	3180
GAAAGATACT TGCTGATTGA CTTCAAGTTC TACTGCTTTC CTCCTAAAAT TATGCATTT	3240
TACAAGACCA TGGGACTTGT GTTGGCTTTA GATCCTGTGC ATCCTGGGCA ACTGTTGTAC	3300
TCTAAGCCAC TCCCCAAAGT CATGCCCGAG CCCCTGTATA ATTCTAAACA ATTAGAATT	3360
TTTCATTT CATTAGTCTA ACCAGGTTAT ATTAATATA CTTAAAGAAA CACCATTGC	3420
CATAAAGTTC TCAATGCCCT TCCCATGCAG CCTCAAGTGG CTCCCCAGCA GATGCATAGG	3480
GTAGTGTGTG TACAAGAGAC CCCAAAGACA TAGAGCCCT GAGAGCATGA GCTGATATGG	3540

Fig.6/3

GGGCTCATAG AGATAGGAGC TAGATGAATA AGTACAAAGG GCAGAAATGG GTTTAACCA	3600
GCAGAGCTAG' AACTCAGACT TTAAAGAAAA TTAGATCAA GTAGAGACTG AATTATTCTG	3660
CACATCAGAC TCTGAGCAGA GTTCTGTTCA CTCAGACAGA AAATGGGTAA ATTGAGAGCT	3720
GGCTCCATTG TGCTCCTTAG AGATGGGAGC AGGTGGAGGA TTATATAAGG TCTGGAACAT	3780
TTAACTTCTC CGTTCTCAT CTTCAAGGG ATACTACAAT TCTGTGGAAT	3840
GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG TATGCAAAGC	3900
ATGCATCTCA ATTAGTCAGC AACCAAGGTGT GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA	3960
AGTATGCAAA GCATGCATCT CAATTAGTCA GCAACCATAG TCCCAGCCCT AACTCCGCC	4020
ATCCCGCCCC TAACTCCGCC CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTT	4080
TTTATTTATG CAGAGGCCGA GGCAGCTCTG AGCTATTCCA GAAGTAGTGA GGAGGCTTT	4140
TTGGAGGCCT AGGCTTTGC AAAAAAGCTA ATTCAAGCTG AATGGCGAAT GGGACGCGCC	4200
CTGTAGCGGC GCATTAAGCG CGGCAGGGTGT GGTGGTTACG CGCAGCGTGA CCGCTACACT	4260
TGCCAGCGCC CTAGCGCCCG CTCCCTTCGC TTTCTCCCT TCCTTCTCG CCACGTTCGC	4320
CGGCTTCCC CGTCAAGCTC TAAATCGGGG GCTCCCTTA GGGTTCCGAT TTAGTGCTTT	4380
ACGGCACCTC GACCCCAAAA ACTTGATTAG GGTGATGGTT CACGTAGTGG GCCATCGCCC	4440
TGATAGACGG TTTTCGCC TTTGACGTTG GAGTCCACGT TCTTTAATAG TGGACTCTTG	4500
TTCCAAACTG GAACAACACT CAACCCTATC TCGGTCTATT CTTTGATTT ATAAGGGATT	4560
TTGCCGATTT CGGCCTATTG GTTAAAAAAT GAGCTGATTT AACAAAAATT TAACCGGAAT	4620
TTTAACAAAA TATTAACGTT TACAATTCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA	4680
ACCCCTATTG GTTTATTTT CTAAATACAT TCAAATATGT ATCCGCTCAT GAGACAATAA	4740
CCCTGATAAA TGCTTCAATA ATATTGAAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT	4800
GTCGCCCTTA TTCCCTTTT TGCGGCATT TGCCCTCCTG TTTTGCTCA CCCAGAAACG	4860
CTGGTGAAAG TAAAAGATGC TGAAGATCAG TTGGGTGCAC GAGTGGGTTA CATCGAACTG	4920
GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTCGCCCCG AAGAACGTTT TCCAATGATG	4980
AGCACTTTA AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTATTGACGC CGGGCAAGAG	5040
CAACTCGGTC GCCGCATAACA CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTCACA	5100
GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT GCAGTGCTGC CATAACCAG	5160
AGTGATAACA CTGCGGCCAA CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAAC	5220
GCTTTTGC ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG	5280
AATGAAGCCA TACCAAAACGA CGAGCGTGAC ACCACGATGC CTGTAGCAAT GGCAACAAACG	5340

Fig.6/4

08/484.312

TTGCGCAAAC TATTAACTGG CGAACTACTT ACTCTAGCTT CCCGGCAACA ATTAATAGAC	5400
TGGATGGAGG' CGGATAAAAGT TGCAGGACCA CTTCTGCGCT CGGCCCTTCC GGCTGGCTGG	5460
TTTATTGCTG ATAAATCTGG AGCCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG	5520
GGGCCAGATG GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGAG TCAGGCAACT	5580
ATGGATGAAC GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA	5640
CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT TAAAACCTCA TTTTTAATT	5700
AAAAGGATCT AGGTGAAGAT CCTTTTGAT AATCTCATGA CCAAAATCCC TTAACGTGAG	5760
TTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA AAGGATCTTC TTGAGATCCT	5820
TTTTTCTGC GCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTACC AGCGGTGGTT	5880
TGTTTGCAGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG	5940
CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACCT CAAGAACTCT	6000
GTAGCACCAGC CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC	6060
GATAAGTCGT GTCTTACCGG GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG	6120
TCGGGCTGAA CGGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA	6180
CTGAGATACC TACAGCGTGA GCATTGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGCG	6240
GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGGA GCTTCCAGGG	6300
GGAAACGCCT GGTATCTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA	6360
TTTTGTGAT GCTCGTCAGG GGGCGGGAGC CTATGGAAAA ACGCCAGCAA CGCC	

Fig.7A

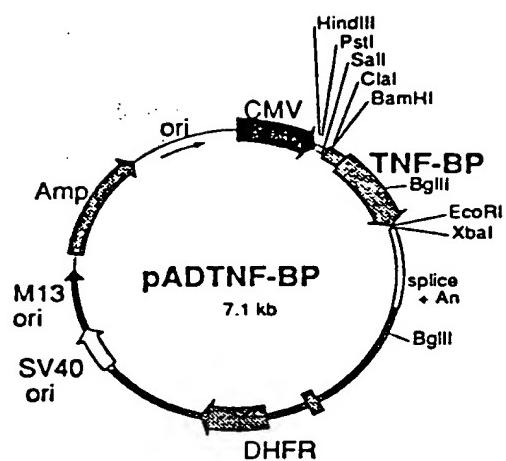


Fig.7B

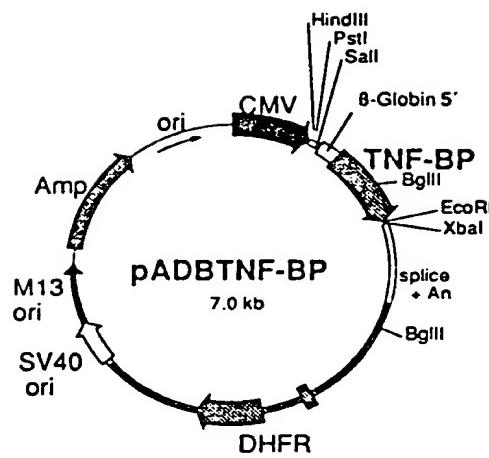


Fig.7C

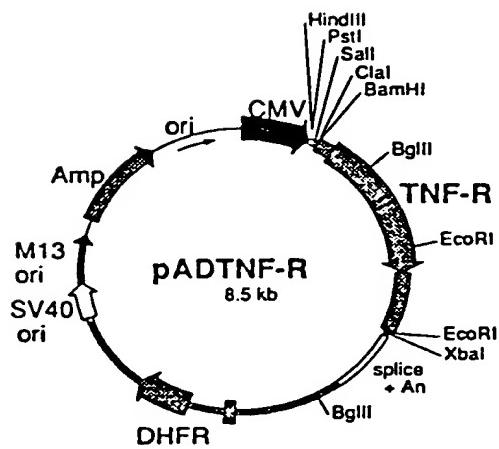
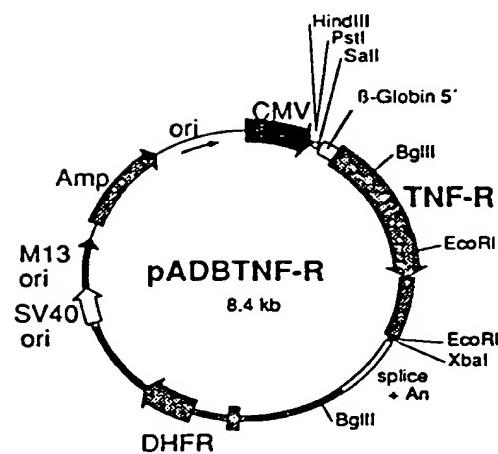


Fig.7D



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Fig.8/1

raTNF-R

GAATTCCTT TCTCCGAGTT TTCTGAACTC TGGCTCATGA TCGGGCTTAC TGGATACGAG	60
AATCTGGAG, GACCGTACCC TGATTTCCAT CTACCTCTGA CTTTGAGCCT TTCTAACCCG	120
GGGCTCACGC TGCCAACACC CGGGCCACCT GGTCCGATCG TCTTACTTCA TTCACCAGCG	180
TTGCCAATTG CTGCCCTGTC CCCAGCCCCA ATGGGGGAGT GAGAGAGGCC ACTGCCGGCC	240
GGAC	
245/1	275/11
ATG GGT CTC CCC ATC GTG CCT GGC CTG CTG CTG TCA CTG GTG CTC CTG GCT CTG CTG ATG	
Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu Leu Ala Leu Leu Met	
305/21	335/31
GGG ATA CAC CCA TCA GGG GTC ACC GGA CTG GTT CCT TCT CTT GGT GAC CGG GAG AAG AGG	
Gly Ile His Pro Ser Gly Val Thr Gly Leu Val Pro Ser Leu Gly Asp Arg Glu Lys Arg	
365/41	395/51
GAT AAT TTG TGT CCC CAG GGA AAG TAT GCC CAT CCA AAG AAT AAT TCC ATC TGC TGC ACC	
Asp Asn Leu Cys Pro Gln Gly Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr	
425/61	455/71
AAG TGC CAC AAA GGA ACC TAC TTG GTG AGT GAC TGT CCA AGC CCA GGG CAG GAA ACA GTC	
Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val	
485/81	515/91
TGC GAG CTC TCT CAT AAA GGC ACC TTT ACA GCT TCG CAG AAC CAC GTC AGA CAG TGT CTC	
Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val Arg Gln Cys Leu	
545/101	575/111
AGT TGC AAG ACA TGT CGG AAA GAA ATG TTC CAG GTG GAG ATT TCT CCT TGC AAA GCT GAC	
Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln Val Glu Ile Ser Pro Cys Lys Ala Asp	
605/121	635/131
ATG GAC ACC GTG TGT GGC TGC AAG AAG AAC CAA TTC CAG CGC TAC CTG AGT GAG ACG CAT	
Met Asp Thr Val Cys Gly Cys Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His	
665/141	695/151
TTC CAG TGT GTG GAC TGC AGC CCC TGC TTC AAT GGC ACC GTG ACA ATC CCC TGT AAG GAG	
Phe Gln Cys Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys Glu	
725/161	755/171
AAA CAG AAC ACC GTG TGT AAC TGC CAC GCA GGA TTC TTT CTA AGC GGA AAT GAG TGC ACC	
Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly Asn Glu Cys Thr	
785/181	815/191
CCT TGC AGC CAC TGC AAG AAA AAT CAG GAA TGT ATG AAG CTG TGC CTA CCT CCA GTT GCA	
Pro Cys Ser His Cys Lys Asn Gln Glu Cys Met Lys Leu Cys Leu Pro Pro Val Ala	
845/201	875/211
AAT GTC ACA AAC CCC CAG GAC TCA GGT ACT GCC GTG CTG TTG CCT CTG GTT ATC TTC CTA	
Asn Val Thr Asn Pro Gln Asp Ser Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu	
905/221	935/231
GGT CTT TGC CTT TTA TTC TTT ATC TGC ATC AGT CTA CTG CGA TAT CCC CAG TGG AGG	
Gly Leu Cys Leu Leu Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg	
965/241	995/251
CCC AGG GTC TAC TCC ATC ATT TGT AGG GAT TCA GCT CCT GTC AAA GAG GTG GAG GGT GAA	
Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys Glu Val Glu Gly Glu	
1025/261	1055/271
GGA ATT GTT ACT AAG CCC CTA ACT CCA GCC TCT ATC CCA GCC TTC AGC CCC AAC CCC GGC	
Gly Ile Val Thr Lys Pro Leu Thr Pro Ala Ser Ile Pro Ala Phe Ser Pro Asn Pro Gly	
1085/281	1115/291
TTC AAC CCC ACT CTG GGC TTC AGC ACC ACC CCA CGC TTC AGT CAT CCT GTC TCC AGT ACC	
Phe Asn Pro Thr Leu Gly Phe Ser Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr	
1145/301	1175/311
CCC ATC AGC CCC GTC TTC GGT CCT AGT AAC TGG CAC AAC TTC GTG CCA CCT GTA AGA GAG	
Pro Ile Ser Pro Val Phe Gly Pro Ser Asn Trp His Asn Phe Val Pro Pro Val Arg Glu	
1205/321	1235/331
GTG GTC CCA ACC CAG GGT GCT GAC CCT CTC CTC TAC GGA TCC CTC AAC CCT GTG CCA ATC	
Val Val Pro Thr Gln Gly Ala Asp Pro Leu Leu Tyr Gly Ser Leu Asn Pro Val Pro Ile	
1265/341	1295/351
CCC GCC CCT GTT CGG AAA TGG GAA GAC GTC GTC GCG GCC CAG CCA CAA CGG CTT GAC ACT	

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Fig.8/2

Pro Ala Pro Val Arg Lys Trp Glu Asp Val Val Ala Ala Gln Pro Gln Arg Leu Asp Thr
 1325/361 1355/371
 GCA GAC CCT GCG ATG CTG TAT GCT GTG GTG GAT GGC GTG CCT CCG ACA CGC TGG AAG GAG
 Ala Asp Pro Ala Met Leu Tyr Ala Val Val Asp Gly Val Pro Pro Thr Arg Trp Lys Glu
 1385/381 1415/391
 TTC ATG CGG CTC CTG GGG CTG AGC GAG CAC GAG ATC GAG CGG CTG GAG CTG CAG AAC GGG
 Phe Met Arg Leu Leu Gly Leu Ser Glu His Glu Ile Glu Arg Leu Glu Leu Gln Asn Gly
 1445/401 1475/411
 CGT TGC CTC CGC GAG GCT CAT TAC AGC ATG CTG GAA GCC TGG CGG CGC CGC ACA CCG CGA
 Arg Cys Leu Arg Glu Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg Arg Thr Pro Arg
 1505/421 1535/431
 CAC GAG GCC ACG CTG GAC GTA GTG GGC CGC GTG CTT TGC GAC ATG AAC CTG CGT GGC TGC
 His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu Cys Asp Met Asn Leu Arg Gly Cys
 1565/441 1595/451
 CTG GAG AAC ATC CGC GAG ACT CTA GAA AGC CCT GCC CAC TCG TCC ACG ACC CAC CTC CCG
 Leu Glu Asn Ile Arg Glu Thr Leu Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro
 1625/461
 CGA TAA
 Arg Stop

GGCCACACCC CCACCTCAGG AACGGGACTC GAAGGACCAT CCTGCTAGAT	1680
GCCCTGCTTC CCTGTGAACC TCCTCTTGG TCCTCTAGGG GGCAGGCTCG ATCTGGCAGG	1740
CTCGATCTGG CAGCCACTTC CTTGGTGCTA CCGACTTGGT GTACATAGCT TTTCCCAGCT	1800
GCCGAGGACA GCCTGTGCCA GCCACTTGTG CATGGCAGGG AAGTGTGCCA TCTGCTCCC	1860
GACAGCTGAG GGTGCCAAAA GCCAGGAGAG GTGATTGTGG AGAAAAAGCA CAATCTATCT	1920
GATAACCACT TGGGATGCAA GGACCCAAAC AAAGCTCTC AGGGCCTCCT CAGTTGATT	1980
CTGGGCCCTT TTCACAGTAG ATAAAACAGT CTTGTATTG ATTATATCAC ACTAATGGAT	2040
GAACGGTTGA ACTCCCTAACG GTAGGGGCAA GCACAGAAC A GTGGGGTCTC CAGCTGGAGC	2100
CCCCGACTCT TGTAAATACA CTAAAAATCT AAAAGTGA AAAAAAAAAA AAAAAAAAAA	2160
AAAAAAAGGAA TTC	

Fig.9/1

huTNF-R

GAATTCTCTG, GACTGAGGCT CCAGTTCTGG CCTTTGGGGT TCAAGATCAC TGGGACCAGG	60
CCGTGATCTC TATGCCCGAG TCTCAACCT CAACTGTCAC CCCAAGGCAC TTGGGACGTC	120
CTGGACAGAC CGAGTCCCAG GAAGCCCCAG CACTGCCGCT GCCACACTGC CCTGAGCCCA	180
AATGGGGGAG TGAGAGGCCA TAGCTGTCTG GC	

213/1	243/11
ATG GGC CTC ACC GTG CCT GAC CTG CTG CTG CCA CTG GTG CTC CTG GAG CTG TTG GTG	
Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val	
273/21	303/31
GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA	
Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg	
333/41	363/51
GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC	
Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr	
393/61	423/71
AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC	
Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp	
453/81	483/91
TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC	
Cys Arg Glu Cys Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu	
513/101	543/111
AGC TGC TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC	
Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp	
573/121	603/131
CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG AGT GAA AAC CTT	
Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu	
633/141	663/151
TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG	
Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu	
693/161	723/171
AAA CAG AAC ACC GTG TGC ACC TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC	
Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val	
753/181	783/191
TCC TGT AGT AAC TGT AAG AAA AGC CTG GAG TGC ACG AAG TTG TGC CTA CCC CAG ATT GAG	
Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu	
813/201	843/211
AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT	
Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe	
873/221	903/231
GGT CTT TGC CTT TTA TCC CTC CTC TTC ATT GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG	
Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys	
933/241	963/251
TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA TCG ACA CCT GAA AAA GAG GGG GAG CTT GAA	
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu	
993/261	1023/271
GGA ACT ACT AAG CCC CTG GCC CCA AAC CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC	
Gly Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr	
1053/281	1083/291
CCC ACC CTG GGC TTC AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC	
Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Thr Tyr Thr	
1113/301	1143/311
CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA CCA CCC TAT CAG GGG	
Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly	
1173/321	1203/331
GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC TCC GAC CCC ATC CCC AAC CCC CTT CAG AAG	
Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys	

B/484312

Fig. 9/2

1233/341	1263/351
TGG GAG GAC AGC GCC CAC AAG CCA CAG AGC	CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC
Trp Glu Asp Ser Ala His Lys Pro Gln Ser	Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr
1293/361	1323/371
GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC	TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG
Ala Val Val Glu Asn Val Pro Pro Leu Arg	Trp Lys Glu Phe Val Arg Arg Leu Gly Leu
1353/381	1383/391
AGC GAC CAC GAG ATC GAT CGG CTG GAG CTG	CAG AAC GGG CGC TGC CTG CGC GAG GCG CAA
Ser Asp His Glu Ile Asp Arg Leu Glu Leu	Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
1413/401	1443/411
TAC AGC ATG CTG GCG ACC TGG AGG CGG CGC	ACG CCG CGG CGC GAG GCC ACG CTG GAG CTG
Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg	Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu
1473/421	1503/431
CTG GGA CGC GTG CTC CGC GAC ATG GAC CTG	CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG
Leu Gly Arg Val Leu Arg Asp Met Asp Leu	Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala
1533/441	1563/451
CTT TGC GGC CCC GCC CTC CCG CCC GCG CCC AGT	1580
Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala Pro	Ser Leu Leu Arg Stop

GGCTGCGCCC CTGCGGGCAG CTCTAAGGAC CGTCCTGCGA	1620
GATCGCCTTC CAACCCCACT TTTTCTGGA AAGGAGGGGT CCTGCAGGGG CAAGCAGGAG	1680
CTAGCAGCCG CCTACTTGGT GCTAACCCCT CGATGTACAT AGCTTTCTC AGCTGCCCTGC	1740
GCGCCGCCGA CAGTCAGCGC TGTGCGCGCG GAGAGAGGTG CGCCGTTGGC TCAAGAGCCT	1800
GAGTGGGTGG TTTGCGAGGA TGAGGGACGC TATGCCCTCAT GCCC GTTTTG GGTGTCTCA	1860
CCAGCAAGGC TGCTCGGGGG CCCCTGGTTC GTCCCTGAGC CTTTTCAACA GTGCATAAGC	1920
AGTTTTTTT GTTTTGTGTT TGTTTTGTT TGTTTTAAA TCAATCATGT TACACTAATA	1980
GAAACTTGGC ACTCCTGTGC CCTCTGCCCTG GACAAGCACA TAGCAAGCTG AACTGTCCCTA	2040
AGGCAGGGGC GAGCACGGAA CAATGGGGCC TTCAGCTGGA GCTGTGGACT TTTGTACATA	2100
CACTAAAATT CTGAAGTTAA AAAAAAAA AAAAGGAATT C	2141

W/484312

Fig.10

